

Query Match	100.0%	Score 1807;	DB 6;	Length 1808;
Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 1807; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

OY	1	aaagagcagcgcctccctccgcgagcgaggaagaagaagaccagagagagag	60
Db	2	AGAGAGCGCTCCCTCCCTCCGGCGAGGAAAGAAAGAAACCCAGAGAGAGAG	61
OY	61	agagatcctcgaacttcctcccgaccattgactgagactgtgtttcaaacaccgt	12
Db	62	AGAGATATCGCACCTTCTCCTCCGACCATTTACTGCGACTGTGTTCACACACCT	12
OY	121	tgatcctaagaaaaagsglaatgagatctgagcaattcgctgagctgcgacctgat	18
Db	122	TGATCCCAACGAAAAAGAGTAATGAGTACTGCGGCAATTCGTGGCGTCCGACTCAT	18
OY	181	ggttgaagaagaaagttgtatttctatgaccctgagtcgycgaattactactatgac	24
Db	182	GGTTGAAAGAAAGAAAGTTTGTATTCTATGACCCCTGAGGTGGCAATTACTACTATGGC	24
OY	241	caagtgatcccatgaaagcccatacgcatcagatgaaacacagccctctcgtctaacac	30
Db	242	CAAGGTATCCCATGAAAGCCCCATCGCATCCGATACACCATAGCCCTCTCGCTACTAC	30
OY	301	ggtctccctcaagatalgaaagttctcaagcccttcctgcgcgcgaaagctgacotcgc	36
Db	302	GGTCTCCTTCAAGCATATGACAGGTTTCAGACCCCTCCCGCCCGGAACGATCTCGC	36
OY	361	cgcttcgaagcgcgaagacatgtctcttctccgcagatbaacccttgaaaccagaa	42
Db	362	CGCTTCACGCCACGACGATGTCTCTTTCCGACCATTAACCCCTGAAACCCAGCA	42
OY	421	gatacgaattcgccaaactaagagcttcaatgtgttgaagaactgcgcgctttgaaggc	48
Db	422	GATCATATTGCCCACTTAAGGCGTTCAATGTGGTGAAGACTGTCCCGTTTGAAGGC	48
OY	481	cttattcctcttgcagaacctatgcgcgaggaactgttggctgctcgttcaagctaac	54
Db	482	CTTATATCTTTGCCAGACCTATCTGGAGATCTGTGGTGGCTCGTCAACCTTAAC	54
OY	541	caagcgctctgcatatbtccatacgaacgagcgctggtgtccctcaacgcttaagaagtc	60
Db	542	CAGCGCTCTGGATATTGCCATCAACGTGGCTGGTGTCTCCATCAACGCTTAAGATGC	60
OY	601	gagcgctctgcttctgttaccgtcaatgatactgctttagtaccctagaagctccctaa	66
Db	602	GAGCGCTCTGGCTTCTGTTAAGTCAATATCTCTTAGCTATCCTAAGAGCTCCTTAAG	66
OY	661	cagcatgagcgtgtccttattgtcgaattgataaccacaagcgsgatgagtgagagag	72
Db	662	CAGCATGAGCGGTCTTATGTCGAATTAATATCCACACAGGGGATGAGTGAAGAG	72
OY	721	gaatttctgcactgaagaaggttbaacgtctcgtttcataaatttgttattcttc	78
Db	722	GCATTTATGCTACTGACAGAGGTTATACGTCTCGTTTATTAATTTGGTGAATTCTTT	78
OY	781	cccggtacaggtlccatcacaagatalagttatgtatgagaaagatcatctctccat	84
Db	782	CCCGGTACAGGTCACTCAAGGATATAGTTATGTGTAAGCGAAAGTACTATTTCTCAAT	84
OY	841	gtacacactgagatgagaaatcgatagatgagatcaatcgttattacaagccatcatg	90
Db	842	GTACACACTGATATGGAATCGAATGAAGACAGTATCATCTGTATTACAAGCCCATATG	90
OY	901	gggaagaattagaaatttccgaaccaagggcctggttatgcaatgtgtgcatacc	96
Db	902	GGGAAAGTTATGAAATTTTCCACACAGGGGCGTGTGATTTCATATGTGTCTACTCC	96
OY	961	ctatctggagatcggttaagttgctcaactcttcaataaaggtcatagctgagagctc	1020

LOCUS	AF014824	1808 bp	mRNA	12-AUG-1997		
DEFINITION	Arabidopsis thaliana histone deacetylase mRNA, complete cds.					
ACCESSION	AF014824					
VERSION	AF014824.1	GI:2318130				
KEYWORDS						
SOURCE	thale cress, Arabidopsis thaliana					
ORGANISM	Arabidopsis thaliana					

REFERENCE	Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
AUTHORS	1 (bases 1 to 1808)
TITLE	Tomihama, T., Shoji, K., Hanyu, H. and Okano, T.
JOURNAL	Characterization of a histone deacetylase (EST G11C37) in Arabidopsis thaliana
REFERENCE	Unpublished
AUTHORS	2 (bases 1 to 1808)
TITLE	Tomihama, T., Shoji, K., Hanyu, H. and Okano, T.
JOURNAL	Direct Submission
FEATURES	Submitted (16-JUL-1997) Department of Biology, Central Research Institute of Electric Power Industry, 1646, Abiko, Chiba 270-11, Japan
source	location/Qualifiers 1. 1808

```

/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/note="EST clone No. C11C37"
143..1648
/codon_start=1
/product="histone deacetylase"
/protein_id="AAB6486.1"
/db_xref="GI:2318131"
/translation="MDTGKSSLASGPDGKRAKVCITYDEGNNTYTGCGHMKPHRIR
MTHALAYCGLLQHMVLPKPPAPRERDLRPHADVSFLRITPTEOQDILRK-
NGEDCPVFDGLISFCQTVAGSGVSGSLNGLDIDAINAGGILHAKKCEAGFCY
VDVILATLELLKQHERVLVDIDIHGGGVGEAFADRVKTVSFHFGGYFPGGAG
IIDIYVGSGKYSYLVPLDDIGIDIDESHLLEPRIMGKVEIFRGAVVILCGDASG
DLGGEFLNLSIKGHAECVAKPMRFSNVPLILLGGGVTINVARCKCTGEGVALSYVED
KMPLEHYEYEGPDYTLHVAAPSNMKNKNSRQLEBEIRNDLIHNLSTQHAASVPEDR
PDPTETPEVDDQDDEGKRNDPDSMDVDVDDKRLPSVKKDEAVDPTRKDGKIGIM
EGKCKCEVEDESSCTVYGVNVAEASVAKMEEGTNKGKAGAEQAPFPT"

```

Db 962 CTATCTGGGATCGTTAGCTTCTCAATCTTTCATCAAGATCATGCTAGTGCCTC 1021  
QY 1021 aaatttaagatcgttcaatgttccctacgtctctggtggtggttacctatc 1080  
Db 1022 AAATTTATGAGATCGTTCAATGTCCCTACTGCTTGGGTGGTTACATATC 1081  
QY 1081 cgaatgttgcctgtctgtctgaagagcttggaattgcaacttggaattgaattga 1140  
Db 1082 CGCAATGTGCCCCGTGTGTGTCTAGAGACTGCAATTGCACTTGGAGTTGAATTGA 1141  
QY 1141 gacaagatgcgagagcatgaataatatacttggltccagactatacaacttcagct 1200  
Db 1142 GACAAGATGCCGAGCATATATATGATACTTTGGCCAGACTATACACTTCAGCTT 1201  
QY 1201 gctccaaglaacatggaataaataaattctcgtaagatgttgaagagattcgaatgac 1260  
Db 1202 GCTCCAGTAACATGGAATAATAAATTCCTGCAGATGCTTGAAGAGATTGCAATGAC 1261  
QY 1261 ctctccacaatctcttaagcttcagcaatgctccaagtgtacatltcaagaaagacca 1320  
Db 1262 CTTCCTCCACATCTCTTAAGCTTCAGCATGCTCCACAGTACCATTTCCAGAAAGACCA 1321  
QY 1321 cctgatacagagatcccgaggttgatggaagacaaagagatggggaataaagatggat 1380  
Db 1322 CTTGATACAGACCTCCGAGGTGATGAGACCAAGAGATGGGATTAAGATGGAT 1381  
QY 1381 ccgattccagacatgagatgtgatgtagccgttaacctataccaagcagaglaaaaaaga 1440  
Db 1382 CCGGATTTCAGACATGATGTGTGATGACCGTAAACCTATACCAAGCAGACTAAAGA 1441  
QY 1441 gaaactgttgaaccagatacaaaagcaagagatgacgtgaagaattatggagcgtga 1500  
Db 1442 GAAGCTGTTGAAACAGATACAAAGGCAAGATGACTGMAAGAAATTATGCAAGCGTGA 1501  
QY 1501 aaagttgtgaggttgaggttgatgagagtggaagcactaaagttacagagatlaacca 1560  
Db 1502 AAAGTTGTGAGGTGAGGTGAGTGAAGTGAAGCACTTAAGGTTACAGAGATAACCA 1561  
QY 1561 gtggaagtgaagaaagcaagtgtgaatlgaaagagaaagaaacaacaaggttgagcg 1620  
Db 1562 GTGGAGTGGAGAGAACACTGTGAATAATGGAAGAGAAAGAAACAAGGCTGGGCG 1621  
QY 1621 gaagagagcgtttccctctaaacataagaatcgagagcttaattcttgctacttttc 1680  
Db 1622 GAGCAGGCGCTTCTCTCTAAACATAGACTGAGACTCTTAATTTCTGTACTTTTC 1681  
QY 1681 tgcctatcaaatgtctgtatgaattctctgagatgtgtgtgtgaagcaactcctcg 1740  
Db 1682 TGTCTATCAAAATGTCTAGTTCTGAGTTCTGAGTTGTGTGTGAAGCACTCCTGTG 1741  
QY 1741 tttaagagatgagcagagatacttattcttgatgctgcgaatgatgatgat 1800  
Db 1742 TTTTAGAGCATTTAGCAGCAGATATGATTTATTCGTTGCAATGTGATGATGATCAT 1801  
QY 1801 atgacaa 1807  
Db 1802 ATGACAA 1808